

In Claim 34, first line, delete "Claim 33" and substitute -- Claim 33 or 65-- therefor.

In Claim 35, second line, delete "Claim 33" and substitute -- Claim 33 or 65--

therefor.

In Claim 40, second line, delete "37 - 39" and substitute -- 37, 38 and 66-- therefor.

Please amend Claims 23 as follows.

A1 Sub B1
23. The method of Claim 1 or 2 wherein said first nucleic acid concentration [can comprise] comprises [about 10^{-21}] 10^{-21} to [about] 10^{-14} mole nucleic acid fragment per 1 to 10,000 microliters.

Please add the following claims.

A2
--51. A linear nucleic acid insert-vector construct with complementary circularization ends, wherein one or both said circularization ends (1) are attached to an enzyme or enzyme complex capable of covalently joining DNA ends, and (2) are at least about 20 base pairs from each end of said nucleic acid insert.

52. A linear nucleic acid insert-vector construct with complementary circularization ends, wherein one or both said circularization ends (1) are attached to an enzyme or enzyme complex capable of covalently joining DNA ends, and (2) are blocked from covalent joining.

53. A linear nucleic acid insert-vector construct with complementary cohesive circularization ends, wherein said cohesive circularization ends (1) are between about 8 and about 50 nucleotides in length, (2) are at least about 20 base pairs from each end of said nucleic acid insert, and (3) do not comprise cohesive ends of a bacteriophage.

Sub B3
54. A linear nucleic acid insert-vector construct with complementary cohesive circularization ends, wherein said cohesive circularization ends (1) are between about 8 and

about 50 nucleotides in length, (2) are at least about 20 base pairs from each end of said nucleic acid insert, and (3) upon hybridization are not substantially covalently joined by ligase.

55. A nucleic acid insert in a circular vector, wherein:

said circular vector has a first nick in one strand which is about 8 to about 50 nucleotides from a second nick in the other strand;

said first nick and said second nick are at least about 20 base pairs from each end of said nucleic acid insert; and

said first nick and said second nick are not substantially covalently joined by ligase.

56. A nucleic acid insert in a circular vector, wherein:

said circular vector has a first nick in one strand which is about 8 to about 50 nucleotides from a second nick in the other strand;

said first nick and said second nick are at least about 20 base pairs from each end of said nucleic acid insert; and

a nucleotide sequence between said first nick and said second nick does not comprise a bacteriophage cos site.

57. A genomic or cDNA library in a linear vector with complementary circularization ends, wherein one or both said circularization ends (1) are attached to an enzyme or enzyme complex capable of covalently joining DNA ends, and (2) are at least about 20 base pairs from each end of said nucleic acid insert .

58. A genomic or cDNA library in a linear vector with complementary circularization ends, wherein one or both said circularization ends (1) are attached to an enzyme or enzyme complex capable of covalently joining DNA ends, and (2) are blocked

from covalent joining.

59. A genomic or cDNA library in a linear vector with complementary cohesive circularization ends, wherein said cohesive circularization ends (1) are between about 8 and about 50 nucleotides in length, (2) are at least about 20 base pairs from each end of a genomic or cDNA insert, and (3) do not comprise cohesive ends of a bacteriophage.

60. A genomic or cDNA library in a linear vector with complementary cohesive circularization ends, wherein said cohesive circularization ends (1) are between about 8 and about 50 nucleotides in length, (2) are at least about 20 base pairs from each end of a genomic or cDNA insert, and (3) upon hybridization are not substantially covalently joined by ligase.

61. A genomic or cDNA library in a circular vector, wherein:

 said circular vector has a first nick in one strand which is about 8 to about 50 nucleotides from a second nick in the other strand;
 said first nick and said second nick are at least about 20 base pairs from each end of a genomic or cDNA insert; and

 said first nick and said second nick are not substantially covalently joined by ligase.

62. A genomic or cDNA library in a circular vector, wherein:

 said circular vector has a first nick in one strand which is about 8 to about 50 nucleotides from a second nick in the other strand;
 said first nick and said second nick are at least about 20 base pairs from each end of a genomic or cDNA insert; and

 a nucleotide sequence between said first nick and said second nick does not comprise a bacteriophage cos site.

63. A genomic or cDNA library in a linear vector, wherein said genomic or cDNA